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Amino Acid Sequence of hPygo2

MAASAPPPPDKLEGGGGPAPPPAPPSTGRKQGKA<u>GLQMKSPEKK</u>

<u>RRKSNTQGPAYSHLTEFAPPPTPMVDHLVASNPFEDD</u>FGAPKVG

VAAPPFLGSPVPFGGFRVQGGMAGQVPPGYSTGGGGGPQPLRRQ

PPPFPPNPMGPAFNMPPQGPGYPPPGNMNFPSQPFNQPLGQNFS

PPSGQMMPGPVGGFGPMISPTMGQPPRAELGPPSLSQRFAQPGA

PFGPSPLQRPGQGLPSLPPNTSPFPGPDPGFPGPGGEDGGKPLN

PPASTAFPQEPHSGSPAAAVNGNQPSFPPNSSGRGGGTPDANSL

APPGKAGGGSGPQPPPGLVY<u>PCGACRSEVNDDQDAILCEASCQK</u>

<u>WFHRECTGMTESAYGLLTTEASAVWACDLCLKT</u>KEIQSVYIREGM

GQLVAANDG

FIG. 1

ALIGNMENT OF HPYGO1 VS HPYGO2

VERSION BLASTP 2.2.6

Sequence 1 gi 19550449 pygopus 1 [Homo sapiens] Length 419 (1 .. 419)
Sequence 2 gi 21594198 Pygopus 2 [Homo sapiens] Length 406 (1 .. 406)

Score = 240 bits (613)

Identities = 161/439 (36%)
Positives = 214/439 (48%)
Gaps = 58/439 (13%)


```
Pygo1:   3   AENSPAPAYKVSSHGGDSGLDG-------LGGPGVQLGSPDKKKRKANTQGPSFPPLSEY 55
             A ++P P K+   GG +            G  G+Q+ SP+KK+RK+NTQGP++  L+E+
Pygo2:   2   AASAPPPPDKLEGGGGPAPPPAPPSTGRKQGKAGLQMKSPEKKRRKSNTQGPAYSHLTEF 61

Pygo1:  56   APPPNPNSDHLVAANPFDDNYNTISYKPLPSSNPYLGPGYPGFGGYSTFR-MPPHVPPRM 114
             APPP P  DHLVA+NPF+D++   + K   ++ P+LG  P FGG+       M  VPP
Pygo2:  62   APPPTPMVDHLVASNPFEDDFG--APKVGVAAPPFLGSPVP-FGGFRVQGGMAGQVPPGY 118

Pygo1: 115   SSPYCG-PYSLRNQPHPFPQNPLGMGFNRP-HAFNFGPHDNSSFGNPSYNNALSQNVNMP 172
             S+   G P  LR QP PFP NP+G  FN P   + P  N +F + +N  L QN + P
Pygo2: 119   STGGGGGPQPLRRQPPPFPPNPMGPAFNMPPQGPGYPPPGNMNFPSQPFNQPLGQNFSPP 178

Pygo1: 173   NQHFRQNPAENFSQI-------PPQNASQVSNPDLASNFVPGNNSNFTSPLESNHSFIP- 224
             +     P  F +      PP+ +++  P L+  F        SPL+      +P
Pygo2: 179   SGQMMPGPVGGFGPMISPTMGQPPR--AELGPPSLSQRFAQPGAPFGPSPLQRPGQGLPS 236

Pygo1: 225   -PPNTFGQAKAPPPKQDFTQGATKNTNQNSSAHPPHLNMDDTVNQSNIELKNVNRNNAVN 283
             PPNT     +P P D       +     +PP           + A
Pygo2: 237   LPPNT-----SPFPGPDPGFPGPGGEDGGKPLNPP------------------ASTAFP 272

Pygo1: 284   QENSRSSSTEATNNNPANGTQNKPRQPRGAADACTTEKSNKSSLHPNRHGHSSSDP---- 339
             QE  S  ANN +  N   + G DA + K+       G S  P
Pygo2: 273   QEPHSGSPAAAVNGNQPSFPPNSSGRGGGTPDANSLAPPGKAG------GGSGPQPPPGL 326

Pygo1: 340   VYPCGICTNEVNDDQDAILCEASCQKWFHRICTGMTETAYGLLTAEASAVWGCDTCMADK 399
             VYPCG C +EVNDDQDAILCEASCQKWFHR CTGMTE+AYGLLT EASAVW CD C+  K
Pygo2: 327   VYPCGACRSEVNDDQDAILCEASCQKWFHRECTGMTESAYGLLTTEASAVWACDLCLKTK 386
```

PHD-finger.
PHD folds into an i>
330   **

```
Pygo1: 400   DVQLMRTRETFGPSAVGSD 418
             ++Q + RE G     +D
Pygo2: 387   EIQSVYIREGMGQLVAAND 405
```

FIG. 2

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Gal-4

hPygo2 (aa 1-406)

Gal-4-hPygo2-1

Gal-4-hPygo2-2

Gal-4-hPygo2-3

Gal-4-hPygo2-4

Gal-4-hPygo2-5

Gal-4-hPygo2-6

- NLS   - NHD

- Synthetic NLS   - PHD

FIG. 3A

WB:
hPygo2

113 KDa ►
91 ►

50 ►

35 ►

28 ►

FIG. 3B

FIG. 3C

FIG. 3D

FIG. 3E

FIG. 3F

hPygo2 cDNA

FIG. 3G

FIG. 3H

β–Catenin

P-GSK-3 $\begin{matrix}\alpha\\\beta\end{matrix}$ >

GSK-3β

c-Myc

cyclin D1

FIG. 4A

hPygo2   NB

GAPDH

hPygo2   IB

ERK-1
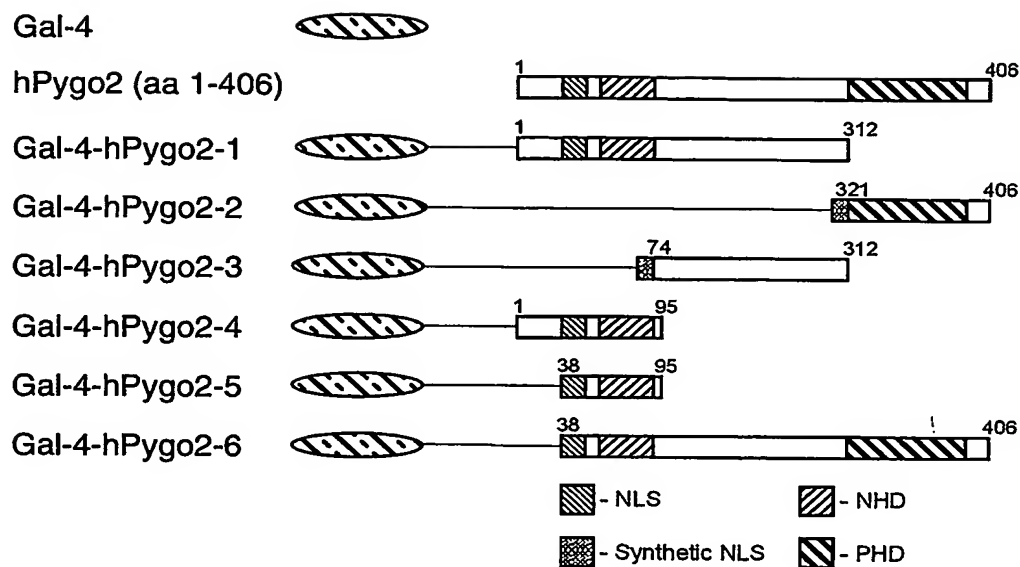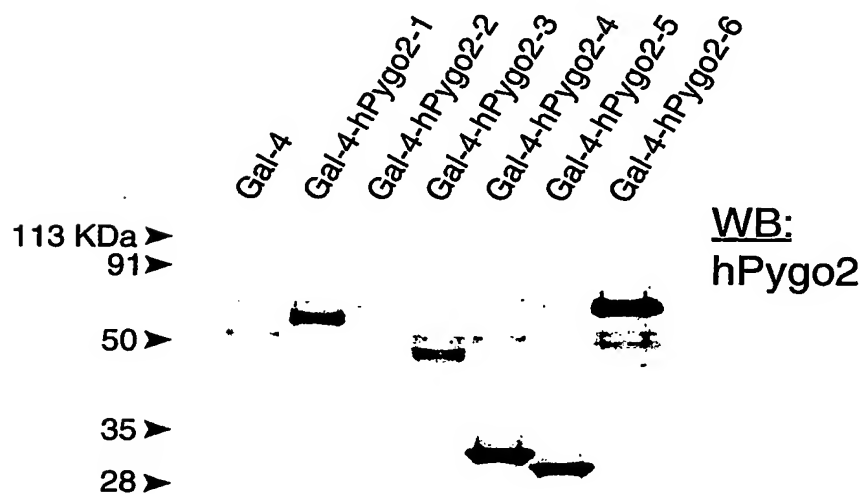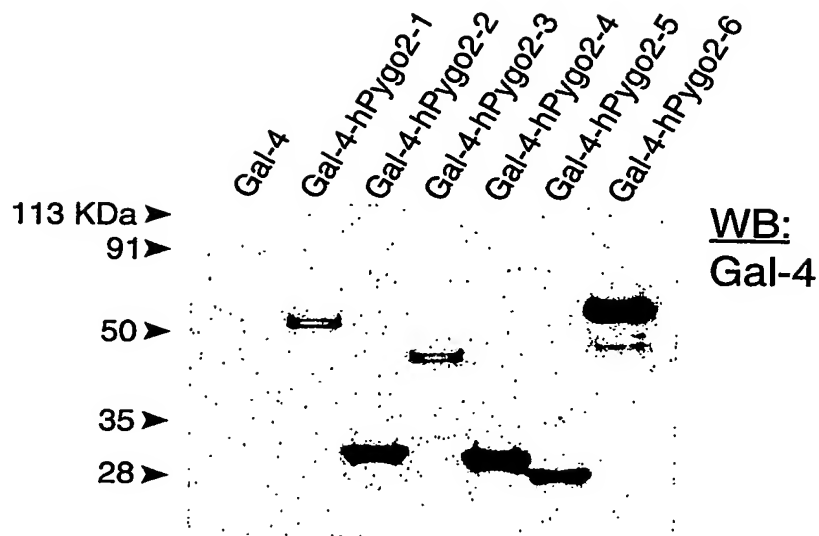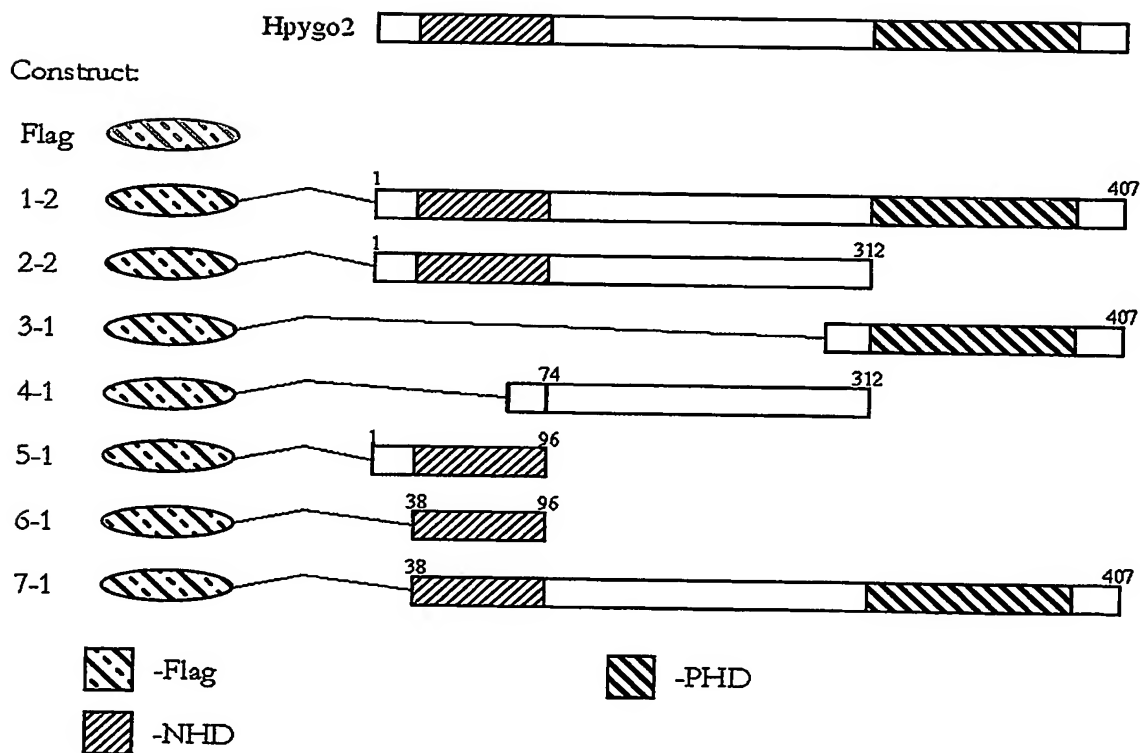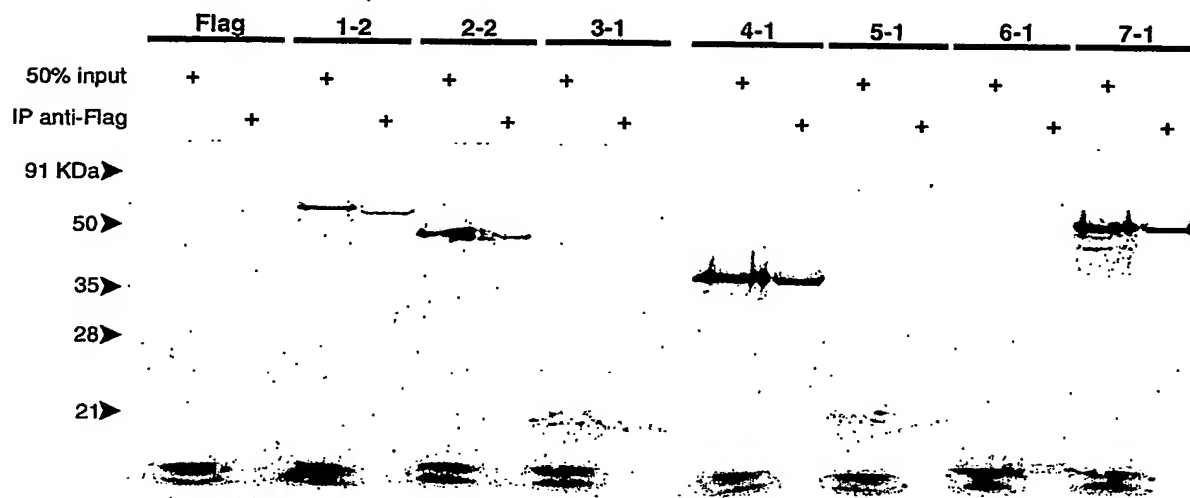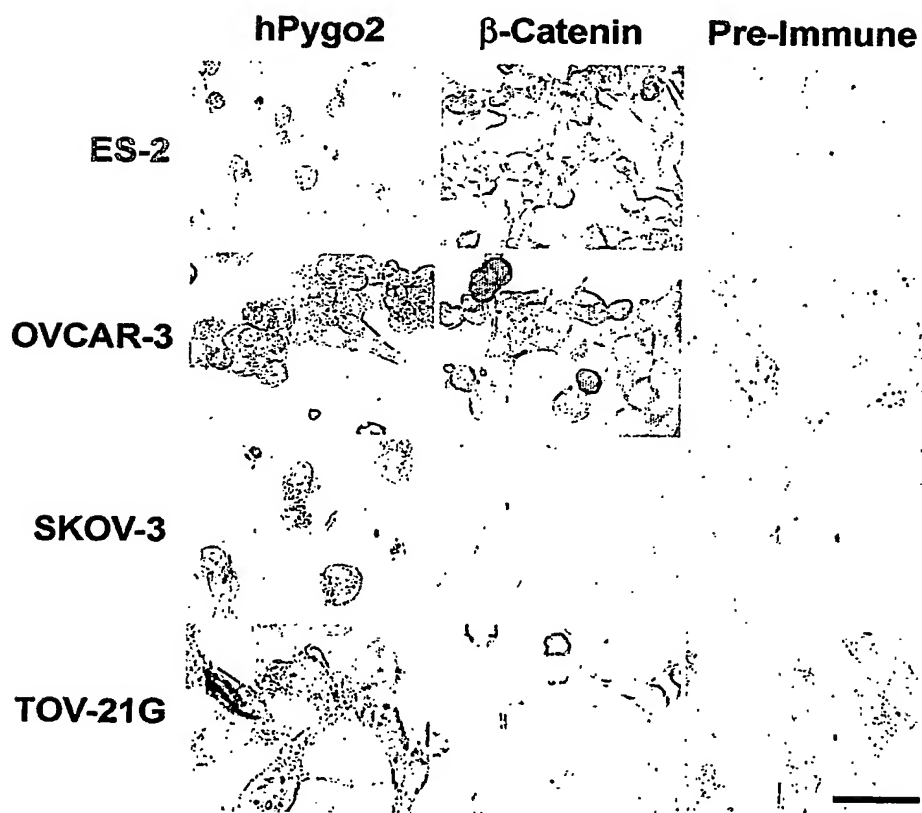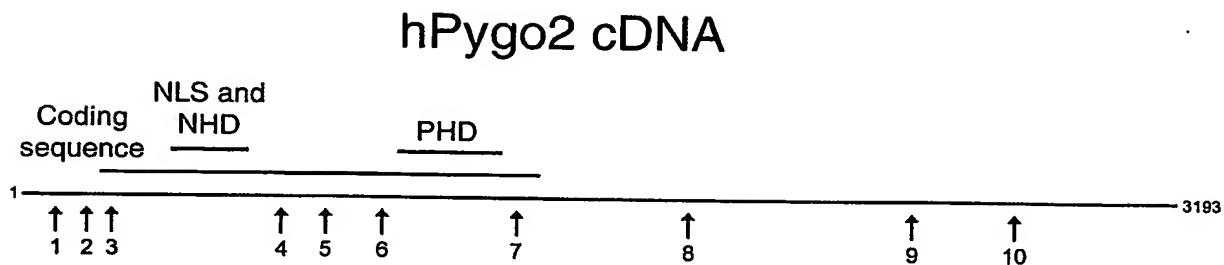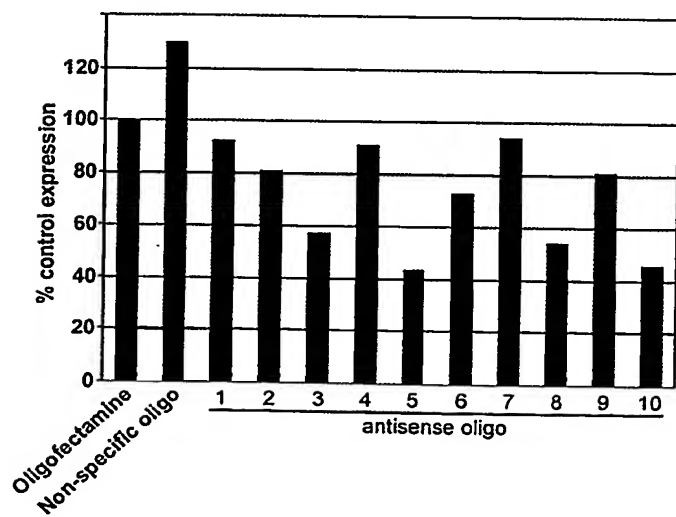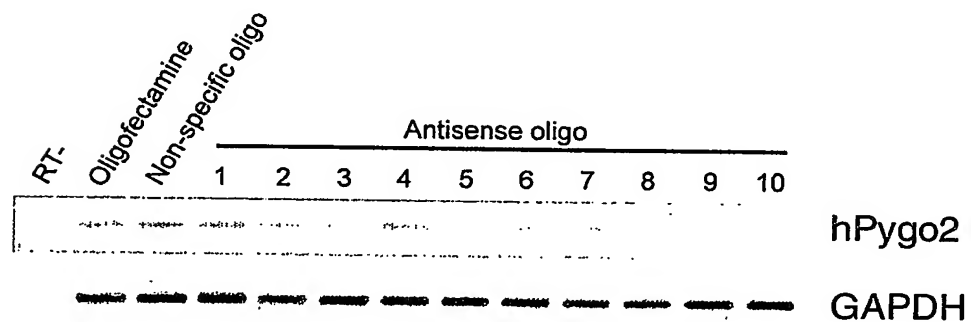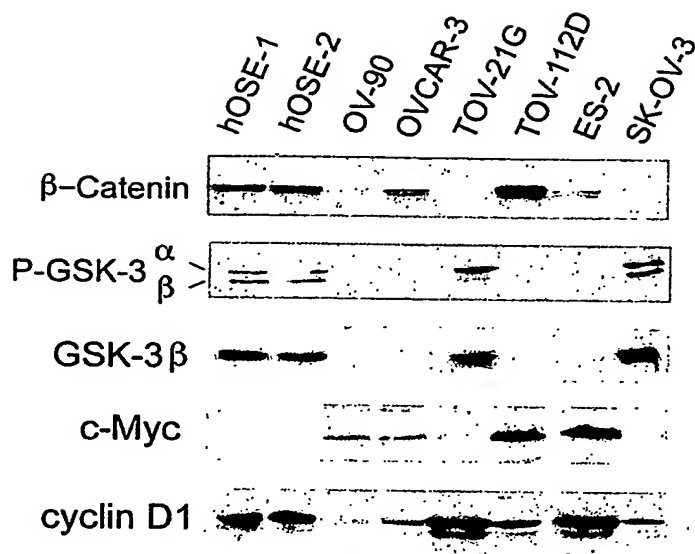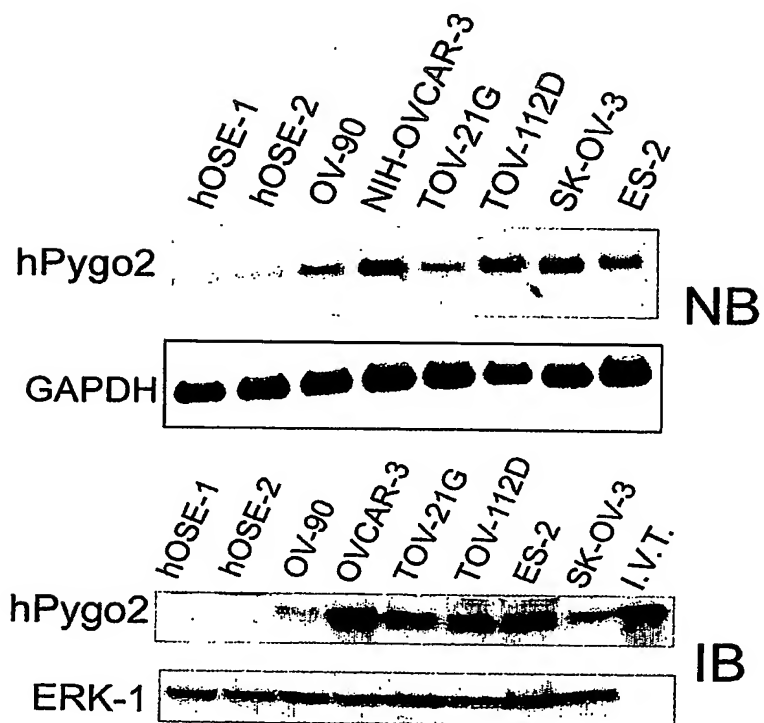
FIG. 4B

8/22
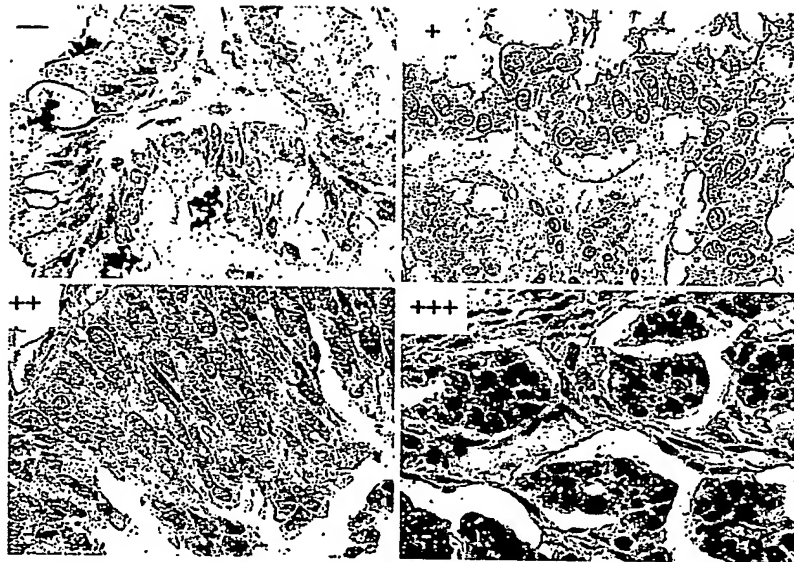
FIG. 4C
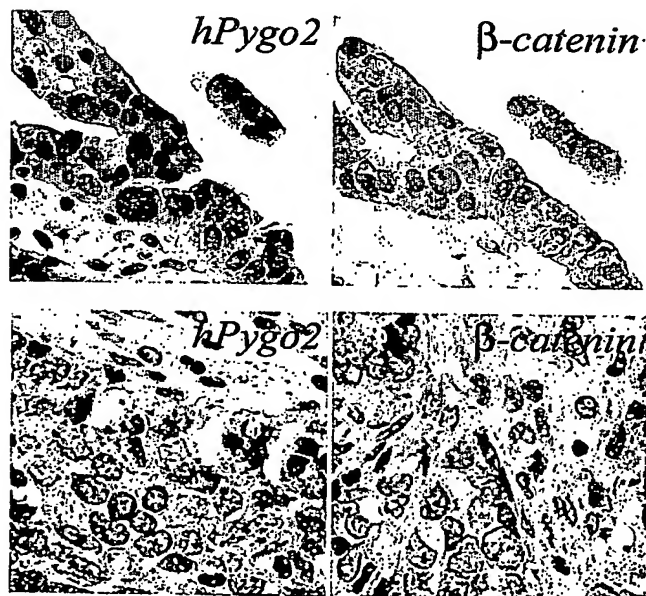
FIG. 4D
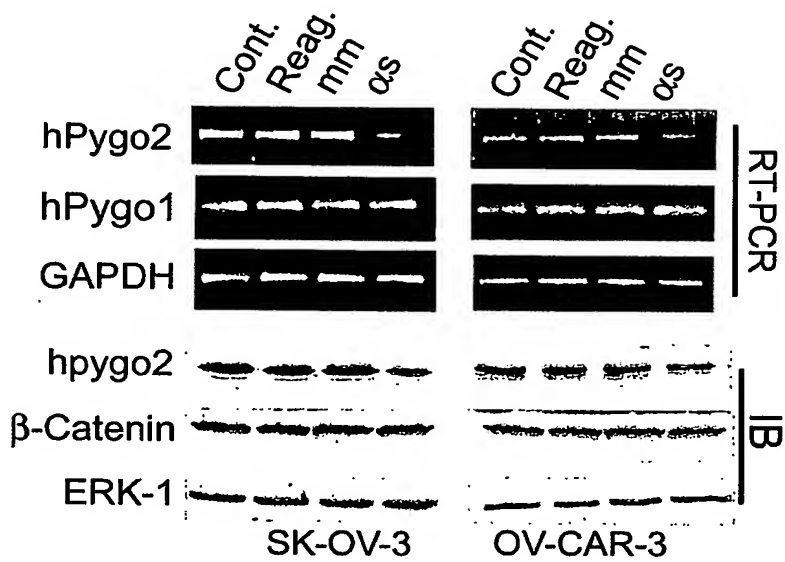
FIG. 5A
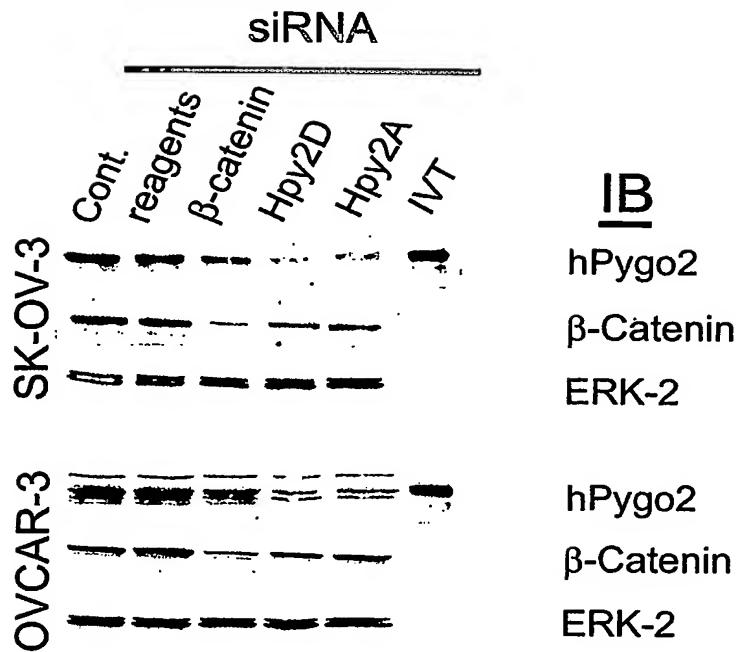
FIG. 5B

FIG. 6A

FIG. 6B

FIG. 6C

FIG. 6D

FIG. 6E

FIG. 6F
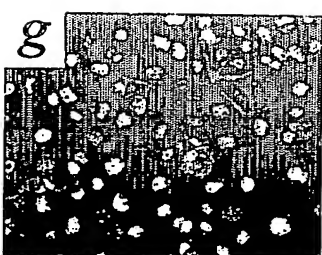
FIG. 6G
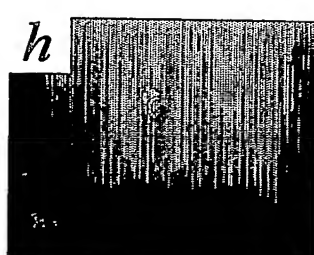
FIG. 6H

FIG. 6I

FIG. 6J

FIG. 6K

FIG. 6L
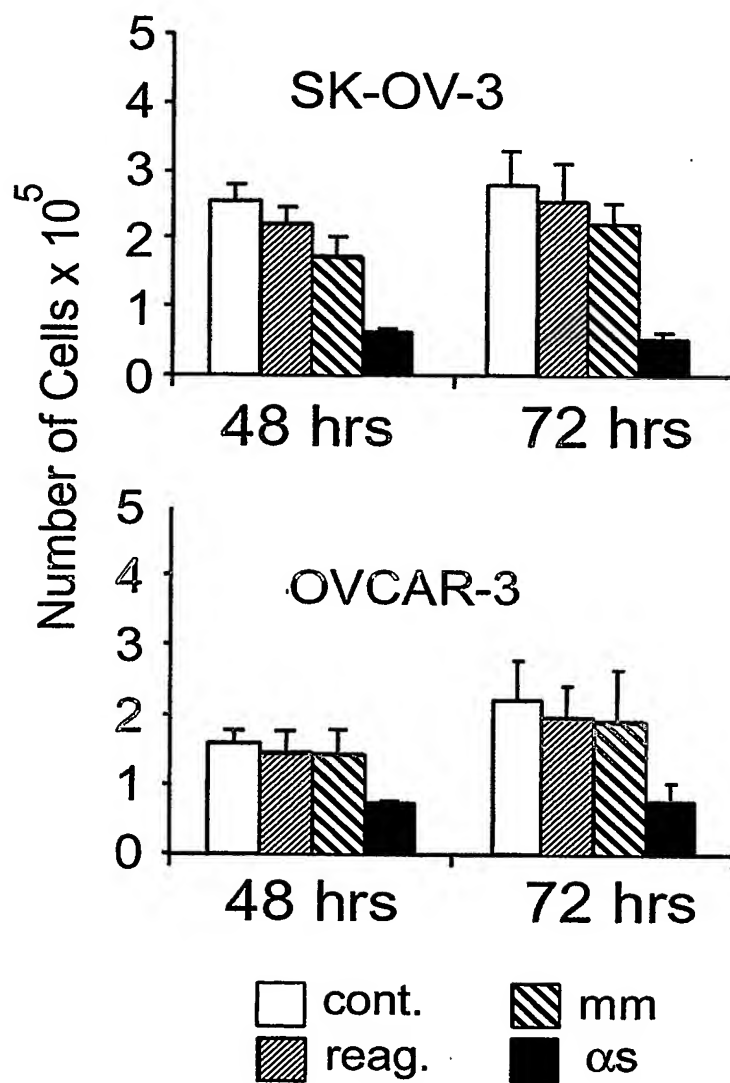
FIG. 7A
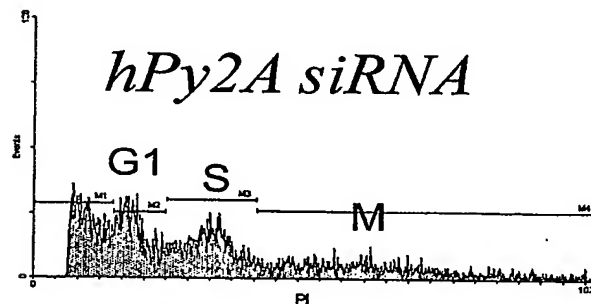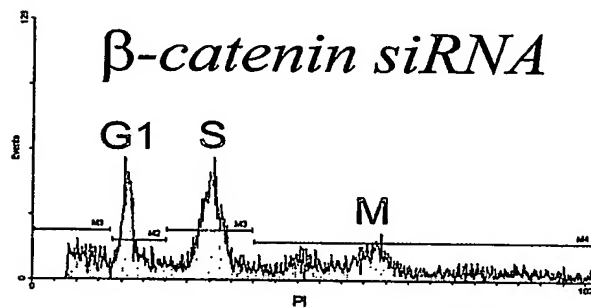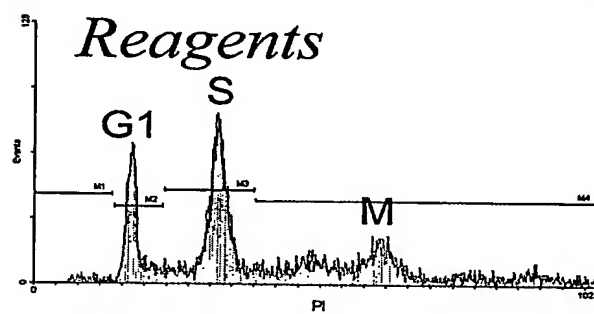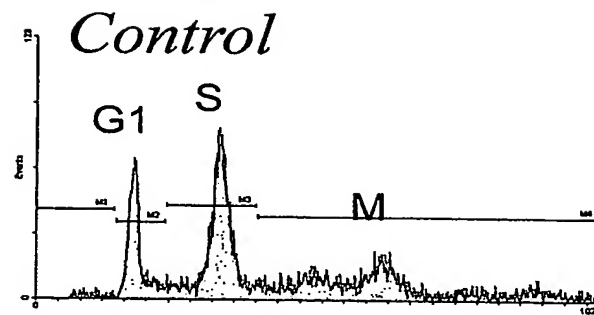
FIG. 7B
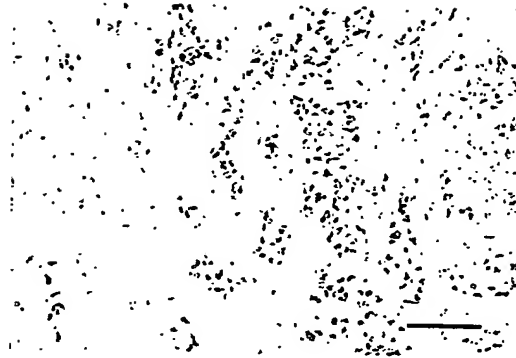
FIG. 8A

FIG. 8B

FIG. 8C

FIG. 8D
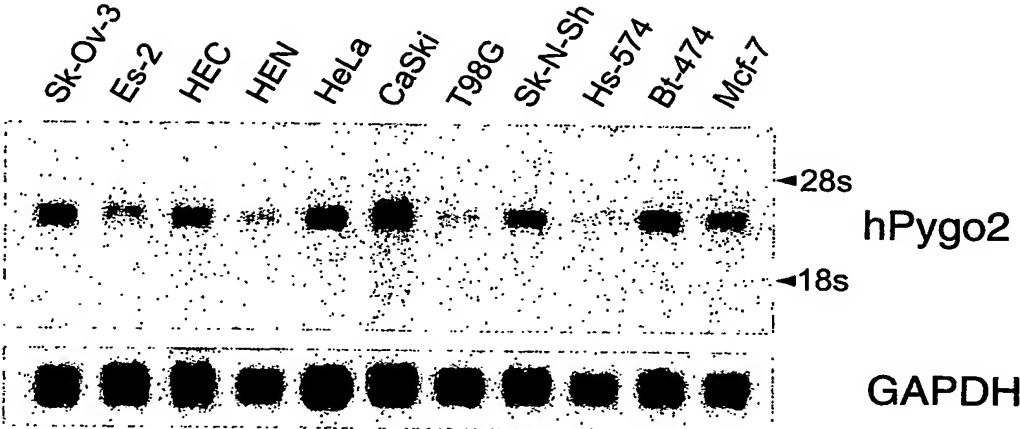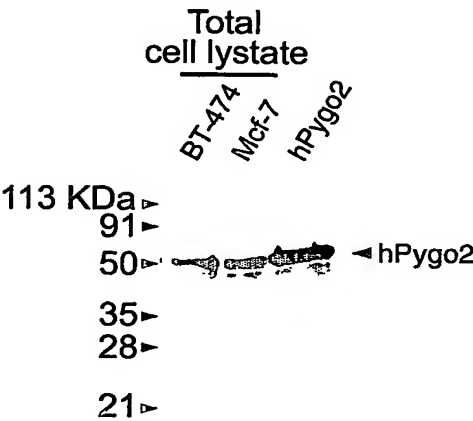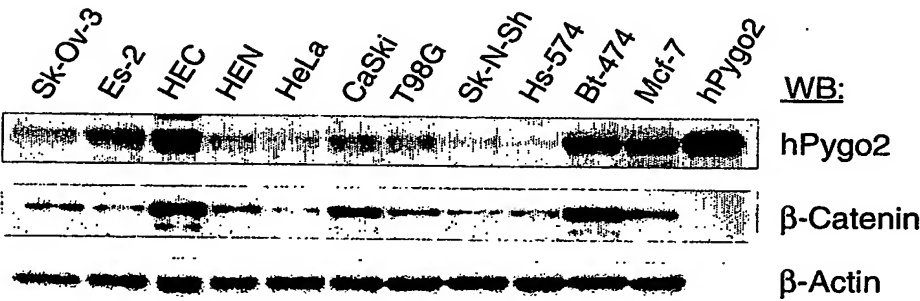
FIG. 9A

FIG. 9B

FIG. 9C

FIG. 9D
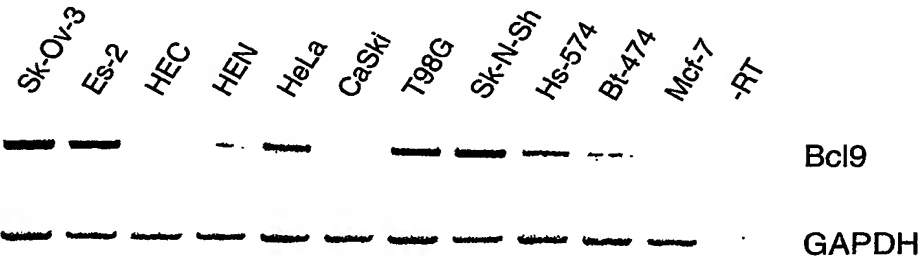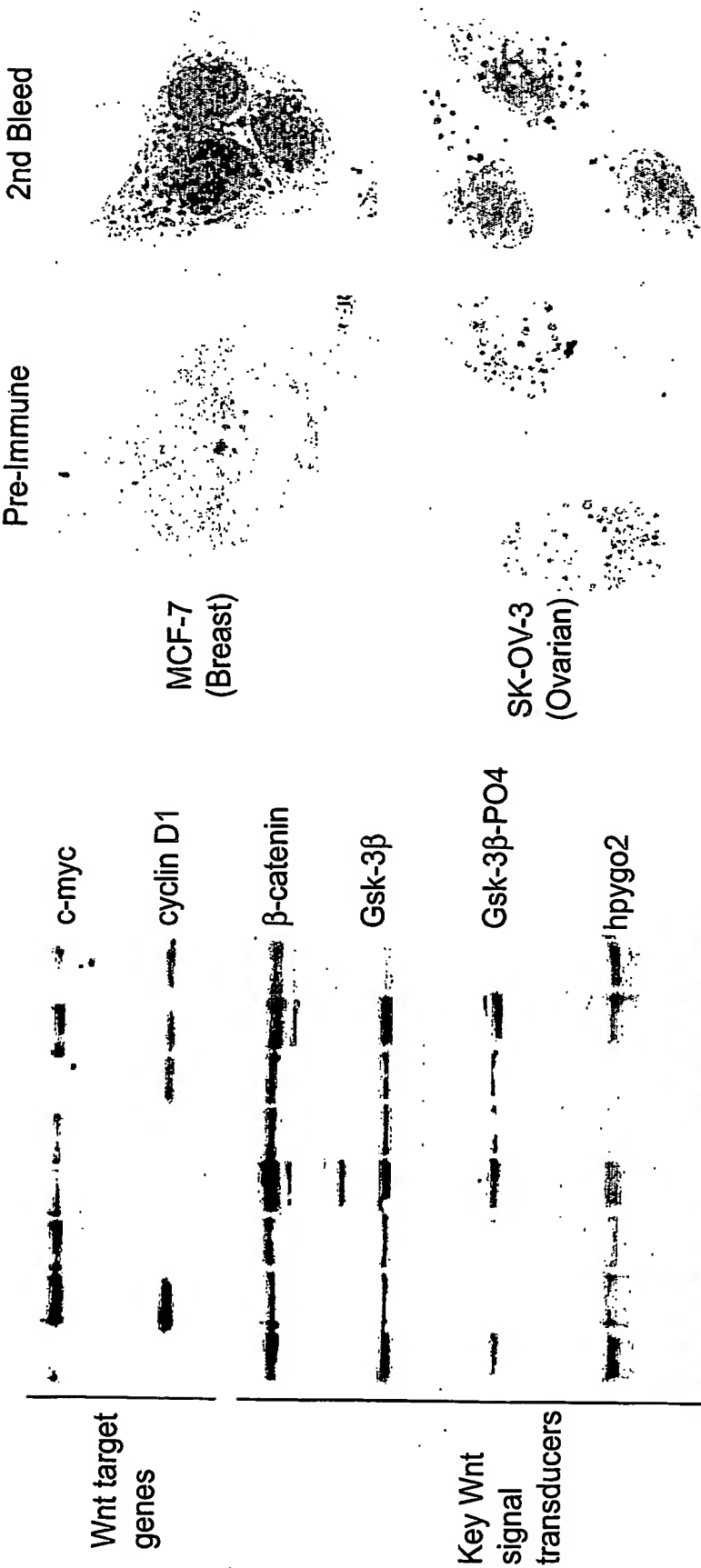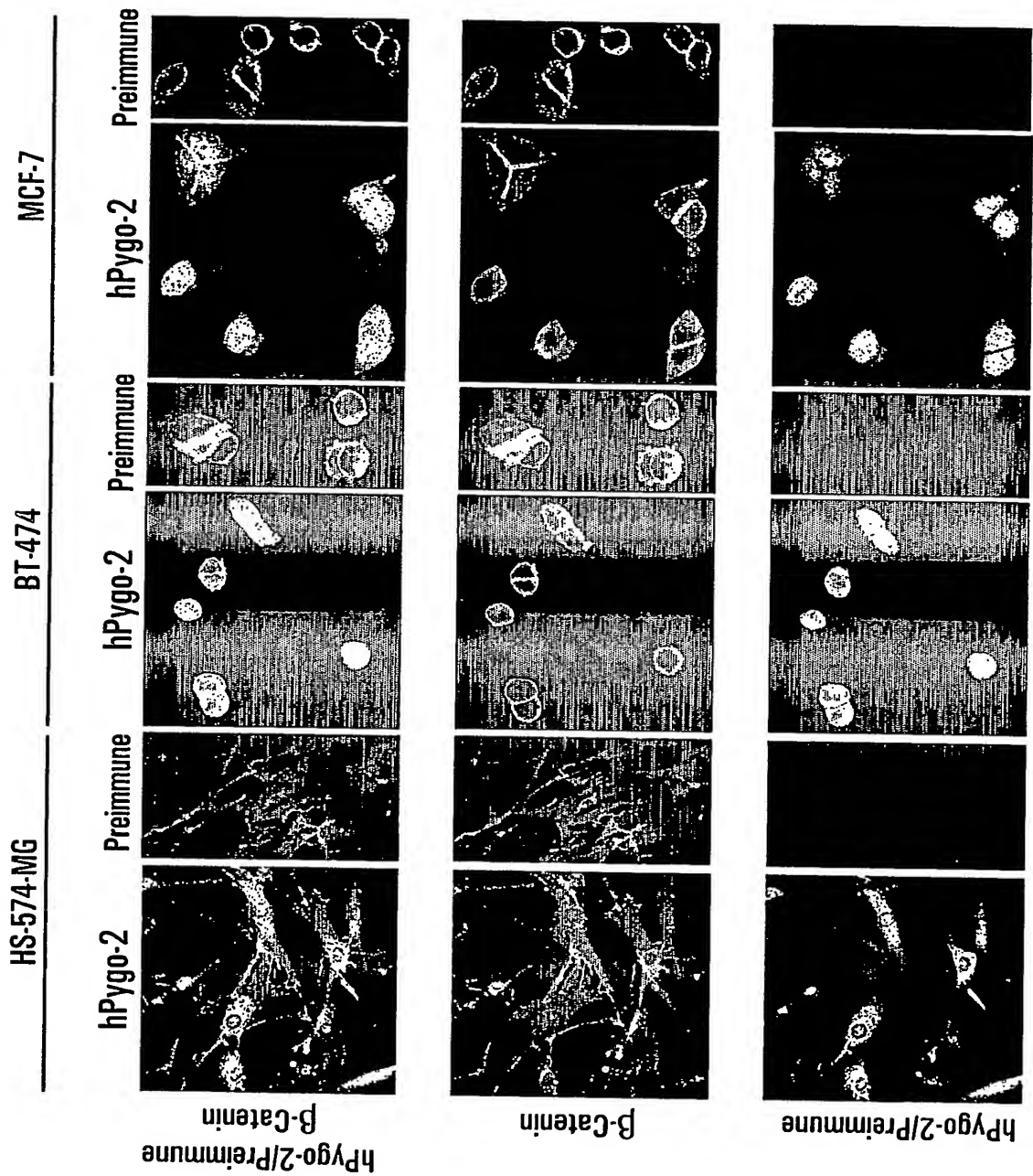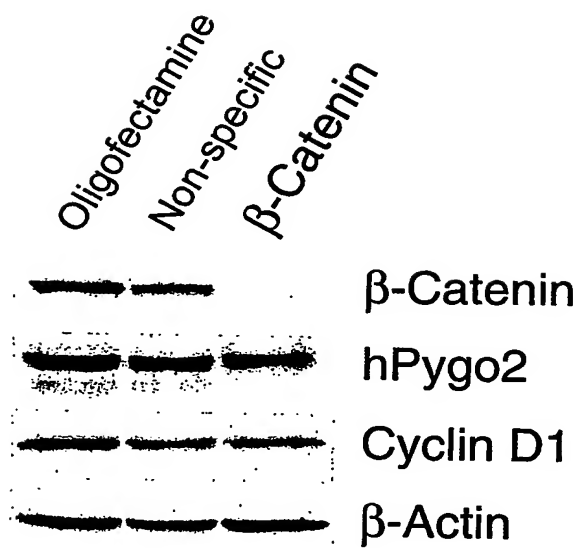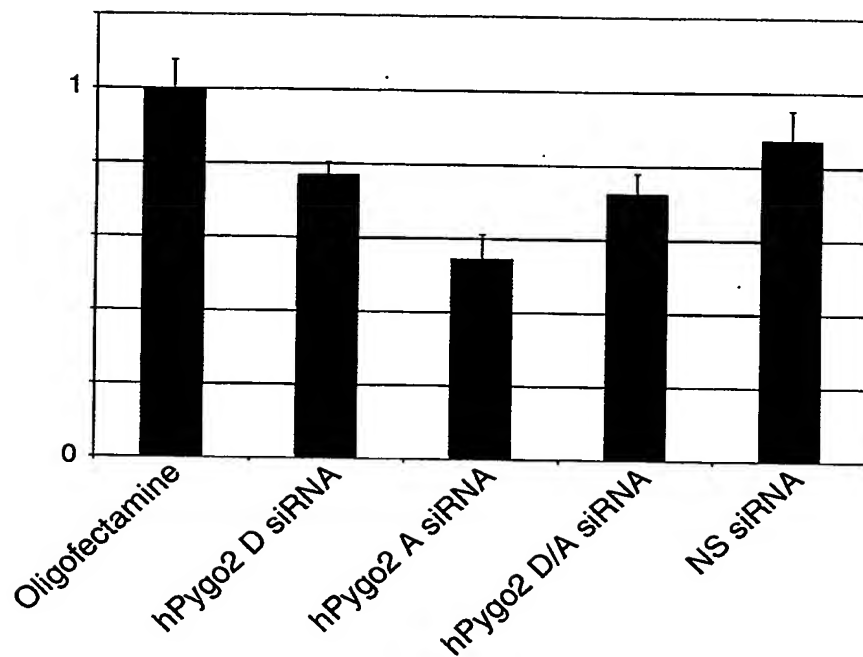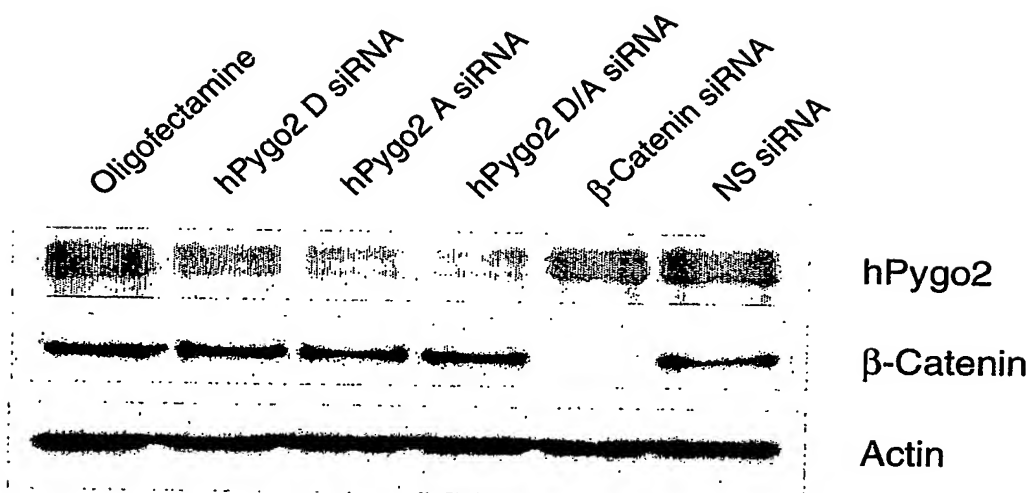
FIG. 9F

FIG. 9E

FIG. 10
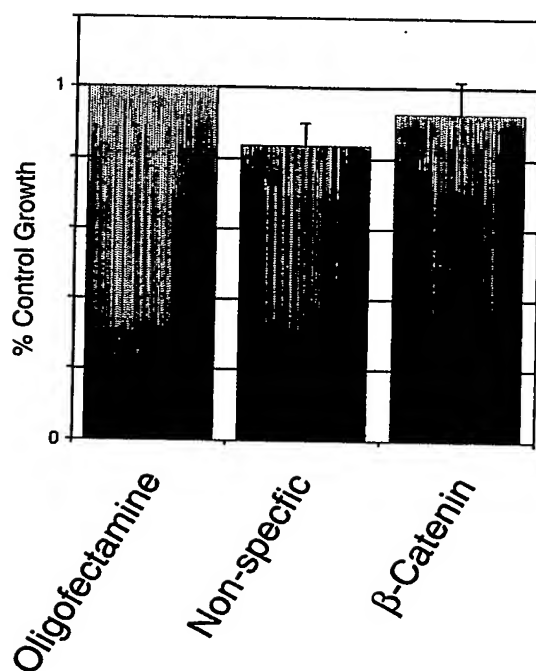
FIG. 11A

FIG. 11B
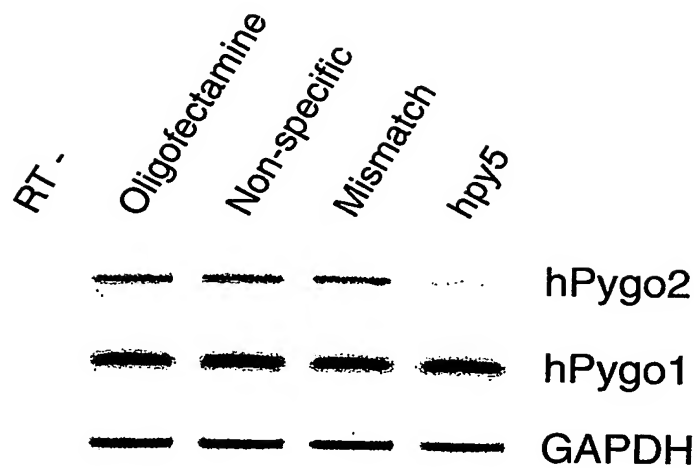
FIG. 12A

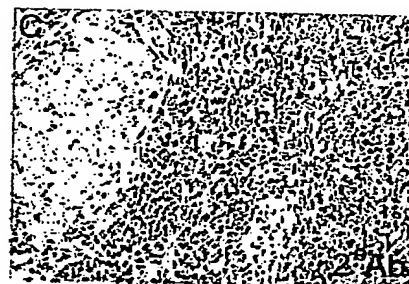FIG. 12B
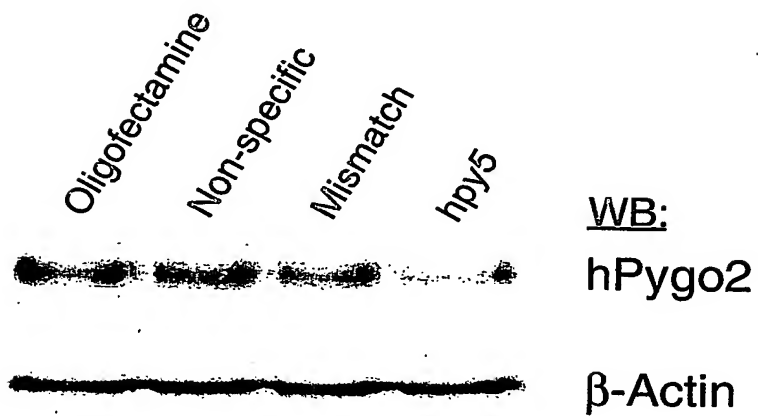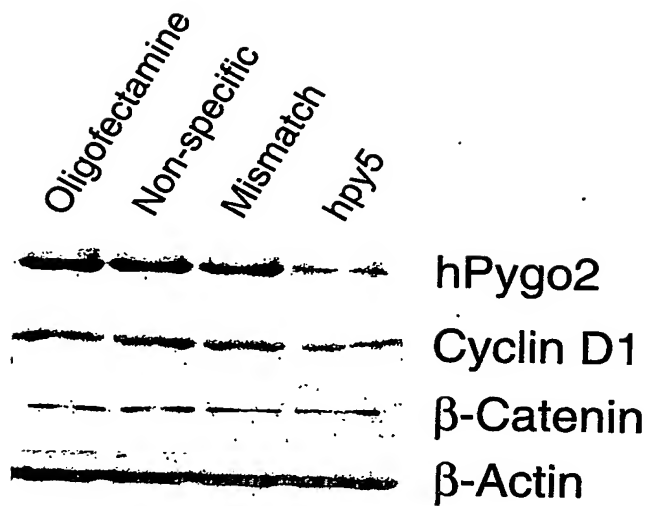
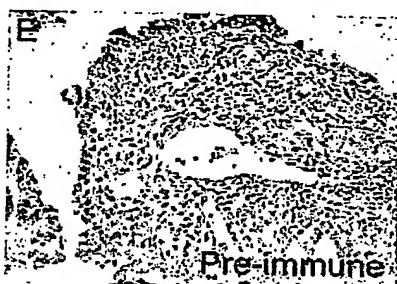FIG. 13A

FIG. 13B
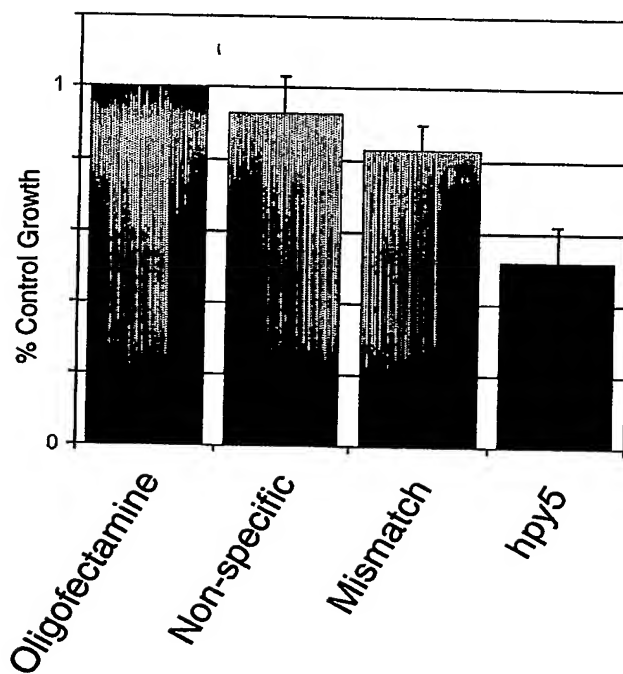
FIG. 14A
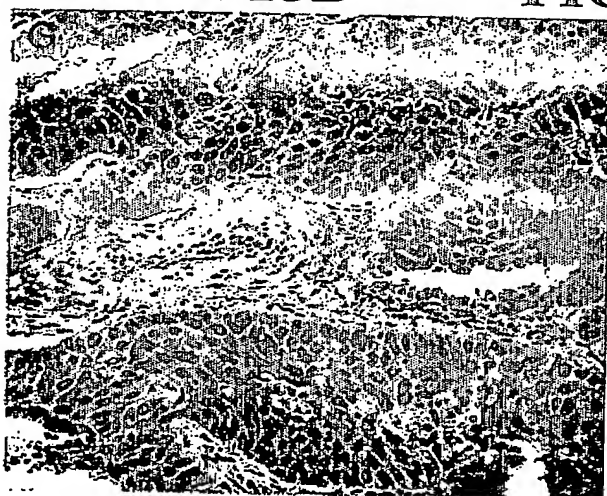

FIG. 14B

FIG. 15A

FIG. 15B

FIG. 15C

FIG. 15D

FIG. 15E

FIG. 15F

FIG. 15G
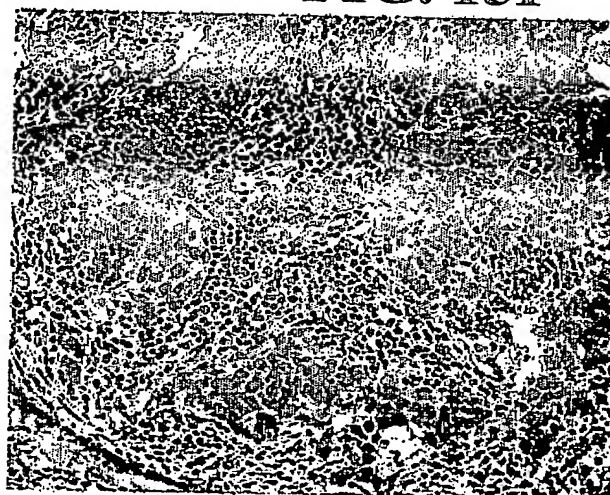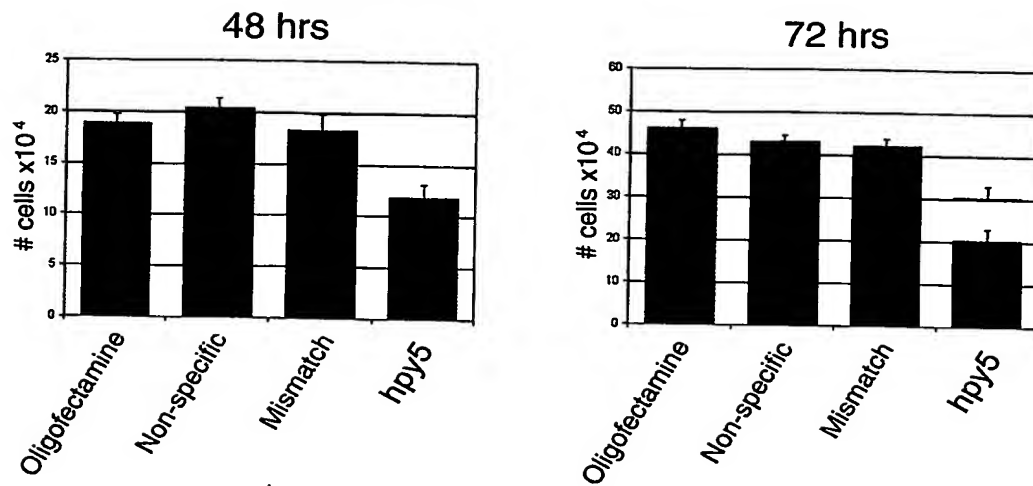
FIG. 15H

FIG. 16A

FIG. 16B

FIG. 16C